

Saving and running a pipeline

By following the steps in this tutorial, you have built a pipeline. You can save this pipeline for future use.

- Select **Create new pipeline** near the bottom left-hand side of the browser window
- Select the **Pre-alignment QA/QC**, **Trim bases**, **Align reads**, **Post-alignment QA/QC**, **Quantify to annotation model**, **Filter features**, **Normalize counts**, **PCA**, and **GSA** task nodes to include them in the pipeline
- Name the pipeline; we have chosen **RNA-Seq basic analysis**
- Give a description for the pipeline; we have noted **trim <20, STAR, normalize with total count and add 0.001, GSA**
- Select **Create pipeline** (Figure 1)

Click on the tasks above to include in the pipeline. Then click **Create pipeline** below.

Pipeline name: Description:

Section name: ▼

Figure 3. Select tasks to include then provide a name and description for the new pipeline

To access this pipeline in the future, select an unaligned reads data node and choose **Pipelines** from the task menu. Available saved pipelines will be available to choose from the *Pipelines* section of the task menu (Figure 2).

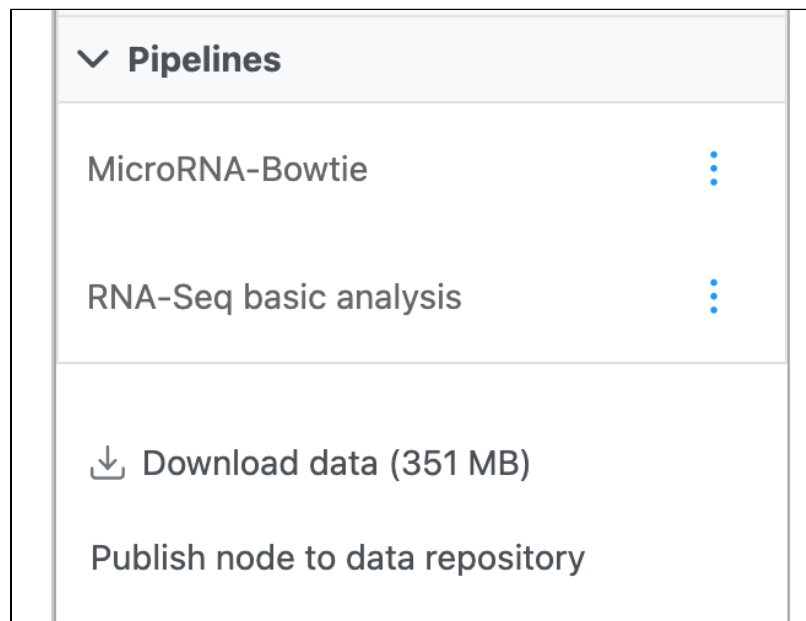


Figure 4. Created pipelines will appear in the *Pipelines* section of the task menu

After selecting the pipeline, you will be prompted to choose the reference genome for alignment, the annotation for quantification, and the contrasts for GSA. After selecting these options, the pipeline will automatically run. See [Pipelines](#) for more information.

Additional Assistance

If you need additional assistance, please visit [our support page](#) to submit a help ticket or find phone numbers for regional support.



Your Rating:



Results:



32 rates